



SEQUENCE LISTING

#4
RECEIVED
DEC 28 2001
TECH CENTER 1600/2900

<120> MAMMALIAN PRO-APOPTOTIC BOK GENES AND
THEIR USES

<130> STAN072CON

<140> 09/682,667

<141> 2001-10-04

<150> 09/517,358

<151> 2000-03-02

<150> 09/186,250

<151> 1998-11-04

<150> 60/064,943

<151> 1997-11-07

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 642

<212> DNA

<213> r. rattus

<400> 1

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gcgcggcttt	tgcgcgccgg	cctctcctgg	agcgtccag	agcgtgcctc	gcctgccct	180
ggaggacgcc	tggcagaggt	gtgcaccgtg	ctgctgcgct	tgggagatga	gctggagcag	240
atccgtccca	gcgtatatcg	gaatgtggcc	cggcagctgc	acatccccct	gcagtctgag	300
cctgtggtga	ctgatgcctt	cctcgctgtg	gccggccaca	tcttctcagc	aggtatcaca	360
tggggcaagg	tagtgtccct	gtactcgggtg	gctgcgggac	tagcgggtgga	ctgcgtccgg	420
caagctcagc	cagccatggg	tcatgccctg	gttgactgcc	tgggggaatt	tgtacgcaag	480
accctggcca	cctggcttcg	gaggcgtggg	ggatggacgg	acgtcctcaa	gtgtgtggtc	540
agcacagacc	ctggcttccg	ctcccactgg	ctcgtggcca	cactctgcag	ctttggccgc	600
ttcctgaagg	ctgcattctt	cctcctgttg	ccagagagat	ga		642

<210> 2

<211> 213

<212> PRT

<213> r. rattus

<400> 2

Met	Glu	Val	Leu	Arg	Arg	Ser	Ser	Val	Phe	Ala	Ala	Glu	Ile	Met	Asp
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		20						25					30		
Ala	Leu	Gly	Arg	Glu	Tyr	Val	His	Ala	Arg	Leu	Leu	Arg	Ala	Gly	Leu
		35					40					45			
Ser	Trp	Ser	Ala	Pro	Glu	Arg	Ala	Ser	Pro	Ala	Pro	Gly	Gly	Arg	Leu
		50				55					60				
Ala	Glu	Val	Cys	Thr	Val	Leu	Leu	Arg	Leu	Gly	Asp	Glu	Leu	Glu	Gln
65					70					75					80
Ile	Arg	Pro	Ser	Val	Tyr	Arg	Asn	Val	Ala	Arg	Gln	Leu	His	Ile	Pro
			85						90					95	
Leu	Gln	Ser	Glu	Pro	Val	Val	Thr	Asp	Ala	Phe	Leu	Ala	Val	Ala	Gly
			100					105					110		
His	Ile	Phe	Ser	Ala	Gly	Ile	Thr	Trp	Gly	Lys	Val	Val	Ser	Leu	Tyr
		115					120						125		
Ser	Val	Ala	Ala	Gly	Leu	Ala	Val	Asp	Cys	Val	Arg	Gln	Ala	Gln	Pro
		130				135					140				
Ala	Met	Val	His	Ala	Leu	Val	Asp	Cys	Leu	Gly	Glu	Phe	Val	Arg	Lys
145					150					155					160
Thr	Leu	Ala	Thr	Trp	Leu	Arg	Arg	Arg	Gly	Gly	Trp	Thr	Asp	Val	Leu
				165					170					175	
Lys	Cys	Val	Val	Ser	Thr	Asp	Pro	Gly	Phe	Arg	Ser	His	Trp	Leu	Val
			180				185					190			
Ala	Thr	Leu	Cys	Ser	Phe	Gly	Arg	Phe	Leu	Lys	Ala	Ala	Phe	Phe	Leu
		195					200					205			
Leu	Leu	Pro	Glu	Arg											
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<210> 3
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 <213> r.rattus

<220>
 <221> CDS
 <222> (1) ... (513)

<400> 3																
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Met	Glu	Val	Leu	Arg	Arg	Ser	Ser	Val	Phe	Ala	Ala	Glu	Ile	Met	Asp	
1				5					10					15		
gcc	ttt	gat	cgc	tcg	ccc	aca	gac	aag	gag	ctg	gtg	gcc	cag	gct	aaa	96
Ala	Phe	Asp	Arg	Ser	Pro	Thr	Asp	Lys	Glu	Leu	Val	Ala	Gln	Ala	Lys	
			20					25					30			
gca	cta	ggc	cgg	gag	tac	gtg	cac	gcg	cgg	ctt	ttg	cgc	gcc	ggc	ctc	144
Ala	Leu	Gly	Arg	Glu	Tyr	Val	His	Ala	Arg	Leu	Leu	Arg	Ala	Gly	Leu	
		35					40					45				
tcc	tgg	agc	gct	cca	gag	cgt	gcc	tcg	cct	gcc	cct	gga	gga	cgc	ctg	192
Ser	Trp	Ser	Ala	Pro	Glu	Arg	Ala	Ser	Pro	Ala	Pro	Gly	Gly	Arg	Leu	
		50				55					60					

gca gag gtg tgc acc gtg ctg ctg cgc ttg gga atc aca tgg ggc aag	240
Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Ile Thr Trp Gly Lys	
65 70 75 80	
gta gtg tcc ctg tac tgc gtg gct gcg gga cta gcg gtg gac tgc gtc	288
Val Val Ser Leu Tyr Ser Val Ala Ala Gly Leu Ala Val Asp Cys Val	
85 90 95	
cgg caa gct cag cca gcc atg gtt cat gcc ctg gtt gac tgc ctg ggg	336
Arg Gln Ala Gln Pro Ala Met Val His Ala Leu Val Asp Cys Leu Gly	
100 105 110	
gaa ttt gta cgc aag acc ctg gcc acc tgg ctt cgg agg cgt ggt gga	384
Glu Phe Val Arg Lys Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly	
115 120 125	
tgg acg gac gtc ctc aag tgt gtg gtc agc aca gac cct ggc ttc cgc	432
Trp Thr Asp Val Leu Lys Cys Val Val Ser Thr Asp Pro Gly Phe Arg	
130 135 140	
tcc cac tgg ctc gtg gcc aca ctc tgc agc ttt ggc cgc ttc ctg aag	480
Ser His Trp Leu Val Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys	
145 150 155 160	
gct gca ttc ttc ctc ctg ttg cca gag aga tga	513
Ala Ala Phe Phe Leu Leu Leu Pro Glu Arg *	
165 170	

<210> 4
 <211> 170
 <212> PRT
 <213> r.rattus

<400> 4
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Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu
35 40 45
Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu
50 55 60
Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Ile Thr Trp Gly Lys
65 70 75 80
Val Val Ser Leu Tyr Ser Val Ala Ala Gly Leu Ala Val Asp Cys Val
85 90 95
Arg Gln Ala Gln Pro Ala Met Val His Ala Leu Val Asp Cys Leu Gly
100 105 110
Glu Phe Val Arg Lys Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly
115 120 125
Trp Thr Asp Val Leu Lys Cys Val Val Ser Thr Asp Pro Gly Phe Arg
130 135 140
Ser His Trp Leu Val Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys

acc ttg gct acc tgg ctt cgg agg cgt ggt gga tgg acg gac gtc ctc	528
Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly Trp Thr Asp Val Leu	
165 170 175	
aag tgt gtg gtc agc aca aaa cct ggc ttc cgc tcc cac tgg ctc gtg	576
Lys Cys Val Val Ser Thr Lys Pro Gly Phe Arg Ser His Trp Leu Val	
180 185 190	
gcc aca ctc tgc agc ttt ggc cgc ttc ctg aag gct gca ttc ttc ctc	624
Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys Ala Ala Phe Phe Leu	
195 200 205	
ctg ttg cca gag aga tga	642
Leu Leu Pro Glu Arg *	
210	

<210> 6
 <211> 213
 <212> PRT
 <213> H.sapiens

<400> 6

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35 40 45	
Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu	
50 55 60	
Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Asp Glu Leu Glu Gln	
65 70 75 80	
Ile Arg Pro Ser Val Tyr Arg Asn Val Ala Arg Gln Leu His Ile Pro	
85 90 95	
Leu Gln Ser Glu Pro Val Val Thr Asp Ala Phe Leu Ala Val Ala Gly	
100 105 110	
His Ile Phe Ser Ala Gly Ile Thr Trp Gly Lys Val Val Ser Leu Tyr	
115 120 125	
Ser Ala Ala Ala Gly Leu Ala Val Asp Cys Val Arg Gln Ala Gln Pro	
130 135 140	
Ala Met Val His Ala Leu Val Asp Cys Leu Gly Glu Phe Val Arg Lys	
145 150 155 160	
Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly Trp Thr Asp Val Leu	
165 170 175	
Lys Cys Val Val Ser Thr Lys Pro Gly Phe Arg Ser His Trp Leu Val	
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195 200 205	
Leu Leu Pro Glu Arg	
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<210> 7
 <211> 513
 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (1)...(513)

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gcc ttt gat cgc tgg ccc aca gac aag gag ctg gtg gcc cag gct aaa      96
Ala Phe Asp Arg Trp Pro Thr Asp Lys Glu Leu Val Ala Gln Ala Lys
          20              25              30

gca cta ggc cgg gag tac gtg cac gcg cgg ctt ttg cgc gcc ggc ctc     144
Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu
          35              40              45

tcc tgg agc gct cca gag cgt gcc tcg cct gcc cct gga gga cgc ctg     192
Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu
          50              55              60

gca gag gtg tgc acc gtg ctg ctg cgc ttg gga atc aca tgg ggc aag     240
Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Ile Thr Trp Gly Lys
          65              70              75              80

gta gtg tcc ctg tac tcg gcg gct gcg gga cta gcg gtg gac tgc gtc     288
Val Val Ser Leu Tyr Ser Ala Ala Ala Gly Leu Ala Val Asp Cys Val
          85              90              95

cgg caa gct cag cca gcc atg gtt cat gcc ctg gtt gac tgc ctg ggg     336
Arg Gln Ala Gln Pro Ala Met Val His Ala Leu Val Asp Cys Leu Gly
          100             105             110

gaa ttt gta cgc aag acc ttg gct acc tgg ctt cgg agg cgt ggt gga     384
Glu Phe Val Arg Lys Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly
          115             120             125

tgg acg gac gtc ctc aag tgt gtg gtc agc aca aaa cct ggc ttc cgc     432
Trp Thr Asp Val Leu Lys Cys Val Val Ser Thr Lys Pro Gly Phe Arg
          130             135             140

tcc cac tgg ctc gtg gcc aca ctc tgc agc ttt ggc cgc ttc ctg aag     480
Ser His Trp Leu Val Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys
          145             150             155             160

gct gca ttc ttc ctc ctg ttg cca gag aga tga                          513
Ala Ala Phe Phe Leu Leu Leu Pro Glu Arg *
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<210> 8
 <211> 170
 <212> PRT
 <213> H. sapiens

<400> 8
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 20 25 30
 Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu
 35 40 45
 Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu
 50 55 60
 Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Ile Thr Trp Gly Lys
 65 70 75 80
 Val Val Ser Leu Tyr Ser Ala Ala Ala Gly Leu Ala Val Asp Cys Val
 85 90 95
 Arg Gln Ala Gln Pro Ala Met Val His Ala Leu Val Asp Cys Leu Gly
 100 105 110
 Glu Phe Val Arg Lys Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly
 115 120 125
 Trp Thr Asp Val Leu Lys Cys Val Val Ser Thr Lys Pro Gly Phe Arg
 130 135 140
 Ser His Trp Leu Val Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys
 145 150 155 160
 Ala Ala Phe Phe Leu Leu Leu Pro Glu Arg
 165 170

<210> 9
 <211> 12
 <212> PRT
 <213> R. rattus

<400> 9
 Leu Leu Arg Leu Gly Asp Glu Leu Glu Gln Ile Arg
 1 5 10

<210> 10
 <211> 12
 <212> PRT
 <213> H. sapiens

<400> 10
 Leu Leu Arg Leu Gly Ile Thr Trp Gly Lys Val Val
 1 5 10

<210> 11
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 <213> Artificial Sequence

<220>

<223> Consensus motif

<400> 11

Leu Arg Arg Ala Gly Asp Glu Phe Glu Arg Tyr Arg Arg
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<210> 12

<211> 4

<212> PRT

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<400> 12

Thr Trp Gly Lys
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<210> 13

<211> 4

<212> PRT

<213> H. sapiens

<400> 13

Asn Trp Gly Arg
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<210> 14

<211> 3

<212> PRT

<213> H. sapiens

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<210> 15

<211> 24

<212> PRT

<213> H. sapiens

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<210> 16

<211> 24

<212> PRT

<213> H. sapiens

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<210> 17
 <211> 13
 <212> PRT
 <213> H. sapiens

<400> 17
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 1 5 10

<210> 18
 <211> 12
 <212> PRT
 <213> H. sapiens

<400> 18
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 1 5 10